Centrum voor Wiskunde en Informatica
REPORT*RAPPORT*

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AM-R9514 1995

Report AM-R9514
ISSN 0924-2953

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A Mechanistic Model to Describe the Spread of Phocid Distemper Virus

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Abstract

1. The 1988 epizootic among seals in N.W. Europe led to the death of more than half of the population. Several researchers have fitted data from the epidemic with the Kermack and McKendrick model for disease spread.
2. We argue that for animals living in herds or colonies, like seals, the mutual contact behaviour is such that this model ought to be applied with special care for the distinction between numbers and densities. This is shown by a mechanistic description of the contacts among seals, which leads us to a different formulation of the standard model.
3. This formulation is useful for the description of epidemics among all kinds of animals living in herds.
4. Further analysis shows that the survival of infected animals has a disproportionately great influence on the intensity of the epidemic.
5. Marine pollution may not only have contributed to the high death rates, but may have intensified the epizootic as well.

AMS Subject Classification (1991): 92D30.
Keywords & Phrases: epizootic, herd, modelling, seal disease

1. Introduction

Recently a lot of research has been performed in analysing information on the phocid distemper viral disease (PDV), which caused a large epidemic among the harbour seals, *Phoca vitulina L.*, in north-western Europe in 1988. During this epizootic, in some areas more than half of the seals died as a result of the infection. Among the many articles written on the subject, a few use mathematical models to describe the epizootiology of this infection.

Heide-Jørgensen and Härkönen (1992a) [10] describe the way data about the epizootic were acquired and analysed and then explain the use of a discrete time stochastic model to find the important features of the epizootic. This model is based on the famous Kermack and McKendrick model (1927) [14] for infectious diseases and includes a latency period. In the estimation of the infection parameters, quite different results were obtained for different colonies. The infection rate p seems to depend on the size of the observed colony, instead of being a constant over all the different colonies as expected. Furthermore a fixed threshold size, below which a 'large' epidemic cannot strike the colony, could not be detected. Observations showed that all colonies in the Kattegat-Skagerrak area were equally afflicted.

Grenfell, Lonergan and Harwood (1992) [7] studied the same model (without a latency period) in a continuous time deterministic version, in order to give predictions on future PDV incidence in the seal population. Damping of new outbreaks was predicted, finally leading to a stable endemic equilibrium. Average data were used for parameter estimates and further data analysis concentrated on regional differences in death rates. The modelling problems as observed by Heide-Jørgensen and Härkönen [10] were not found.

Both studies display the same flaw in the application of a well known model. In their article [14], Kermack and McKendrick describe the contacts between individuals by the law of mass action, which means that the per capita number of contacts per unit of time is proportional to the population density. While using this model, researchers usually (explicitly or implicitly) assume that densities will be proportional to the total population size, which allows them to replace the densities by numbers (Anderson, 1982) [1], the advantage of total numbers being that they are more easily observed or measured. This may be true for certain populations and for controlled laboratory experiments (but see also De Jong, Diekmann and Heesterbeek, (in press) [2]), but it is certainly not correct for seals. Like many other species, seals aggregate in colonies, which allows their viruses to profit from a very high host density. Thus it seems logical that the density within the colony is important, and not the density averaged over the total area of the habitat. Next it seems reasonable to assume that the density of the animals is constant, i.e. independent of the size of the colony. The area occupied by the colony will increase or decrease with the size of the population. When modellers neglect this feature, consistent results may still be found, when the population size is constant during the period of study. However, when we consider an infection inducing high mortality, then these aspects should be kept in mind. We can then no longer apply the Kermack and McKendrick model by simply replacing densities by numbers. Further discussion on contact rates in relation to densities and numbers can be found in Diekmann et al. (in press) [5]; De Jong et al. [2].

In the case of the PDV infection, the total number of seals changes indeed during the epizootic, due to a high death rate. By comparing different colonies one can see that, when ashore, the area occupied by the seals depends on the colony size. It appears that the density of seals is more or less equal in all the colonies. This explains why the critical colony size, below which a large epidemic cannot occur, cannot be found. With Kermack and McKendrick we can conclude that, as an epidemic has occurred, the average density in European seal colonies must be above the critical density. The difficulty in determining parameter values for the seal infection can also be explained by this constant density. Thus, as Heide-Jørgensen and Härkönen suggested themselves (Heide-Jørgensen et al. 1992a [10]; Heide-Jørgensen et al. 1992c [12]), the unexpected results of their parameter estimates are explained by the typical gregarious behaviour of the seals.

Below we will explain a model for epidemic outbreaks in herds, using numbers instead of densities. This model is based on assumptions concerning the contact structure among seals, and clearly fits better to the collected data from the seal epizootic. In the following we first explain the formulation of this model in the context of PDV-infection among harbour seals. Next we show the main features of an epidemic as described by this model and then give parameter estimates from the 1988 data. The model is not restricted to seals, but applies, whenever the per capita number of contacts per unit of time is independent of population size.

2. Materials and methods

On an evolutionary time scale, the seal colonies of NW-Europe may be considered as a single closed population. On the much shorter epidemic time scale, however, this population has the features of a meta-population: there are only few exchanges between the different subpopulations (colonies). Therefore we will concentrate on the dynamics of the epidemic within one colony, which we consider as a homogeneously mixing group.

2.1 Assumptions

The underlying assumptions in the model are:
All seals are supposed to be equally susceptible and equally infectious.
Infectiousness and susceptibility are time independent parameters.
PDV infection is followed either by death or lifelong immunity, like for other morbilli-virus infections.
All the seals come ashore each time the tide goes out.
All seals line up in a row along the shoreline and this row will be formed randomly.
The infection can be transmitted only to direct neighbours of an infectious animal.
There is no migration.
Death other than due to infection is neglected, just like birth, since the epidemic takes place in a relatively short time period, compared to the time scale of demographic turnover.

2.2 Ethology

Usually seals are solitary in the water, where they have their own private fishing routes. Social life, if at all, takes place on haul-out sites; in the Wadden Sea these are the tidal sand banks. When the tide is out and the banks appear, seals aggregate and more or less form a row along the shore. The virus is thought to spread during this resting period on the bank, so to formulate a model we will concentrate on this period.

On the sand banks of the Dutch Waddensea the seals typically form a row along the waterline. All the seals are oriented in the same direction, nearly all of the heads directed to the water edge. The virus is transferred by aerosols secreted while coughing and snarling. Such aerosols can only reach noses of animals very close by, so an infectious seal can only infect its nearest neighbours in the line. Thus the effective density of the animals on the beach is constant and independent of the total number of seals on the bank. When the colony size decreases, the row will become shorter, but still all seals will have two neighbours, except those at the ends, so the force of infection will only depend on proportion of seals that are infectious.

2.3 Modelling contacts

Choose S to represent the number of susceptible seals in the colony. Let I denote the number of infectious and R the number of resistant (immune) animals. N denotes the total number of seals in the colony, therefore $N = S + I + R$. Note that we describe numbers now, not densities. Finally let p denote the probability of disease transmission, when a susceptible and an infectious seal lie next to each other during one low tide period.

Let us imagine that the row of seals makes a circle, which we close with one imaginary 'cardboard' seal (neither susceptible nor infectious). Then the problem of discontinuity at the ends of the row is solved and we can easily calculate the force of infection for an average susceptible within this circle. The probability to be infected by the left neighbour is $p * I/N$, which is equal to the probability of infection by the right neighbour. From the sum we subtract the probability of double infection when both the right and left neighbour are infectious: $p^2 * I/N * (I-1)/(N-1)$. Thus we find the total probability of infection (Q).

$$Q = p\frac{I}{N}(2 - p\frac{I-1}{N-1}) \tag{2.1}$$

As Q is the probability for one susceptible animal to become infected, the product SQ is the expected number of newly infected seals in one tide period. This expression is used in a deterministic model, where SQ will be the rate of decrease for S in time.

To analyse the system thoroughly, a further simplification is made. Suppose p is small, then $(2 - pI/N)$ will be close to 2 and Q is almost equal to $2pI/N$, resulting in an expected number of

(almost) $2pSI/N$ new cases each tide period. Thus we arrive at a simple expression, which can be used to describe the epidemic with a model in terms of ordinary differential equations.

2.4 The model

If α denotes $2p$, β is the probability of dying or recovering in one tide period, and f is the average survival for animals that reach the end of the infectious period, then an epidemic in the seal population can be described by the following system of equations:

$$\frac{dS}{dt} = -\alpha\frac{SI}{N} \tag{2.2}$$

$$\frac{dI}{dt} = \alpha\frac{SI}{N} - \beta I \tag{2.3}$$

$$\frac{dR}{dt} = f\beta I \tag{2.4}$$

$$\frac{dN}{dt} = -(1-f)\beta I \tag{2.5}$$

We derived and analysed this model simultaneously with Lefèvre and Picard (1993) [15] (and Picard and Lefévre, 1993 [16]), who give a detailed analysis of the model.

2.5 Analysis

Important information on the initial phase of an epidemic is given by R_0 which is, by definition, the average number of new infections caused by an average infectious seal living in a completely susceptible population. In this model R_0 is equal to α/β. If R_0 is smaller than or equal to one, the infection will immediately disappear from the population, but if R_0 is larger than one an epidemic may occur.

To investigate the final effects of an epidemic, as described by this model, dS/dN is computed and subsequently the differential equation is solved by separation of variables.

$$\frac{dS}{dN} = \frac{\alpha}{\beta(1-f)}\frac{S}{N} \tag{2.6}$$

$$\frac{(1-f)}{R_0} ln\frac{S(t)}{S(0)} = ln\frac{N(t)}{N(0)} \tag{2.7}$$

It is assumed that at time $t = 0$ all the seals are susceptible, so $N(0) = S(0)$. Call the fraction of the population that survived the epidemic x, and the fraction of the initial population that did not get infected at all y. Then

$$\frac{(1-f)}{R_0} lny = lnx \tag{2.8}$$

Next call $(1-f)\beta/\alpha = \theta$ and take exponentials:

$$x = y^{\theta} \tag{2.9}$$

In general, a law of conservation exists: The fraction of seals dying as a result of the infection will be equal to the total fraction that got infected during the epidemic multiplied with the probability to die due to the infection.

$$(1-x) = (1-y)(1-f) \tag{2.10}$$

The two equations (9) and (10) describe the end effects of an epidemic on a susceptible population. They are used to estimate the value of the parameters R_0 and f for the epidemic of 1988. We can rewrite this as in (11) and (12), which shows the influence of the parameters on the final values. This is graphically represented in Figs 1 and 2.

$$R_0 = (1-f)\frac{ln\frac{x-f}{1-f}}{lnx} \tag{2.11}$$

$$R_0 = \frac{(1-f)lny}{ln(y+f(1-y))} \tag{2.12}$$

3. Results

As Figs 1 and 2 show, with equal parameters, the same fraction of animals will become infected in any colony, independent of its size. Observations show that most of the colonies in the area got affected very after another. Therefore the epidemic will follow the same pattern in the total population as in one single colony. Only the time lapse for the disease to spread around to other colonies may cause a small time delay, compared to an epidemic in one big colony.

Graphical representations of the final values under varying parameter values (Figs 1 and 2) show the influence of the parameters f and R_0 on the outcome of the epidemic. In Fig. (3) the influence of our assumption of constant density within a colony is analysed by making a comparison with a model where density is proportional to the total population size. This clearly shows the disproportionate influence of the death rate $(1-f)$. For low values of R_0 and low survival f (as in the PDV epidemic), the difference is quite substantial.

3.1 Parameter estimates

The parameters are estimated mostly from earlier published data with many different sources and collected in different ways. The data are sorted in different tables, to compare collected data from the same source. Estimates in Table 1a (data from Dietz, Heide-Jørgensen and Härkönen, 1989 [6]) display a large variation, which is probably due to high uncertainty in y, the intensity of the epidemic. In this case y is estimated from the number of pups surviving the epidemic. In Table 1b, x is estimated from extrapolation of countings before 1988, and countings in 1989, shortly after the epidemic (Reijnders and Lankester, 1990 [17]). Here we neglect any pups born during the epizootic in 1988. In Table 1c very rough estimates are used [7]. Estimates for y in Table 1c mainly come from antibody tests in Great Britain (Grenfell, Lonergan and Harwood, 1992 [7], Harwood et al. 1989 [9]).

4. Discussion and Conclusions

As we can see from Figs 1 and 2, the most important parameter in the development of the epizootic is f, the survival probability of infected seals. If survival f is small, more seals will die as a consequence of the infection, but also the total fraction $1-y$ of seals that become infected during the epizootic will be higher, because of a positive feedback in the system: If the survival rate f is low, then the *fraction* of susceptible seals will remain relatively high during the epidemic and therefore the force of infection will also remain at a higher level. With higher survival rates, a susceptible can have more

contacts with immunized (recovered) animals, thus reducing the contacts with infectious individuals, which lowers the force of infection. This is supported by data from Scotland, where, compared to the Wadden Sea, higher survival x was found in combination with lower prevalence of PDV antibodies, i.e. lower y (see table 3).

Previous modelling problems found by Heide-Jørgensen and Härkönen (1992a) [10] are solved now. The new parameter estimates show little variation over the different colonies. A minimal group size needed to allow for an epidemic does not exist, but the seals in general seem to live at densities well above the minimal density needed to sustain an epidemic. An epidemic according to this model will follow the same path in all colonies and populations, independent of their size. In an equal time interval an equal fraction of the population will become infected. Only demographic stochasticity in (very) small groups may cause different results.

However, data from Great Britain show different results (table 3). Only about 15% of the Scottish population died during the epidemic (Thompson and Miller, 1992 [19]), but the intensity of the epidemic was still quite high. Other authors have suggested explanations for this, such as the timing of the infection in relation to seasonal behaviour and the presence of secondary infections [13]. Thompson et al.(1992) [19] concludes that it must have been due to either a mutation of the virus or higher resistance of the Scottish seals against the infection.

Comparison of our parameter estimates in the different areas shows that f displays large variation, while R_0 is quite constant. We conclude that mutation of the virus could hardly have caused the regional differences, since only mutants with higher R_0 have good odds to invade during an epidemic, whereas differences in death rate do not influence the success of a virus on such a short term. Differences in survival can be explained better by different levels of pollution. Hall et al. (1992) [8] postulates that high organochlorine levels were associated with higher mortality from PDV, although a direct link could not be established. Reduction of immune functions of seals feeding from the heavily polluted Baltic sea has already been shown by de Swart et al. (1994) [3] and Ross et al. (1995) [18]. This may cause higher case mortality $1-f$ and possibly also higher susceptibility causing a higher R_0. As pollution is relatively low around Scotland, this could explain why resistance and survival of those seals has been higher. Parameter estimates from the model show that f is much higher and R_0 is even a little less than in the more polluted Wadden Sea, Irish Sea and Kattegat-Skagerrak area. Although the model presented here explains most features of the seal epizootic, other suggested influences as mentioned above should not be ruled out. Further research is needed to clarify this issue.

ACKNOWLEDGEMENT We thank Dennis Mollison for sharing with us his idea to simplify the derivation by introducing an imaginary or 'cardboard' seal.

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5. Figures

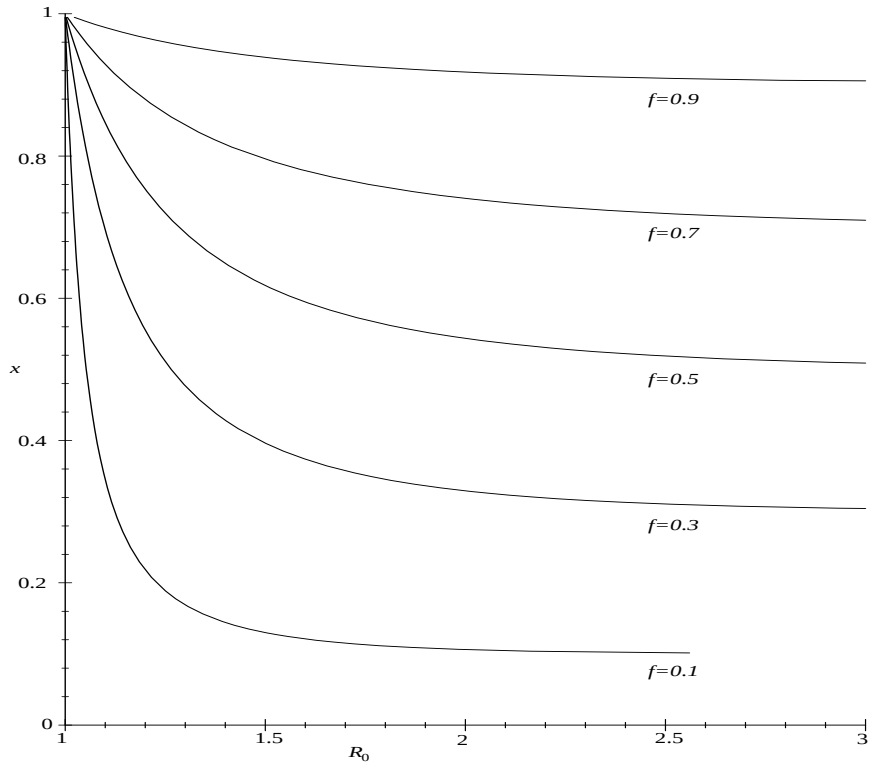

Figure 1. The final fraction of survival of the population, x, as it depends on R_0, the reproduction number of the virus for several survival rates f

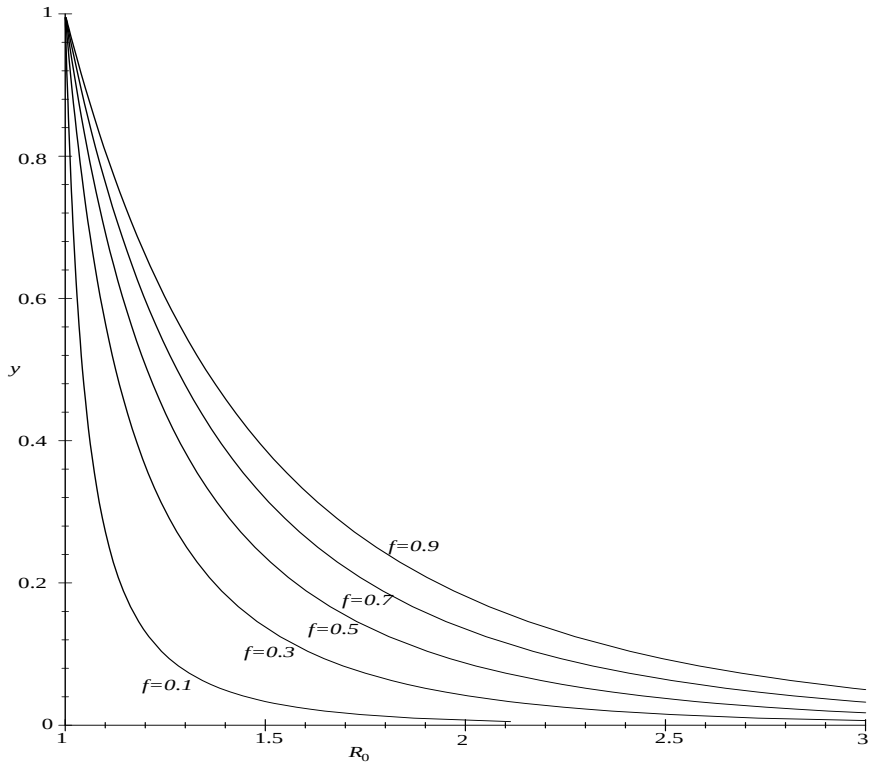

Figure 2. The fraction of the population that remains susceptible, y, as it depends on R_0, the reproduction number of the virus for several survival rates f

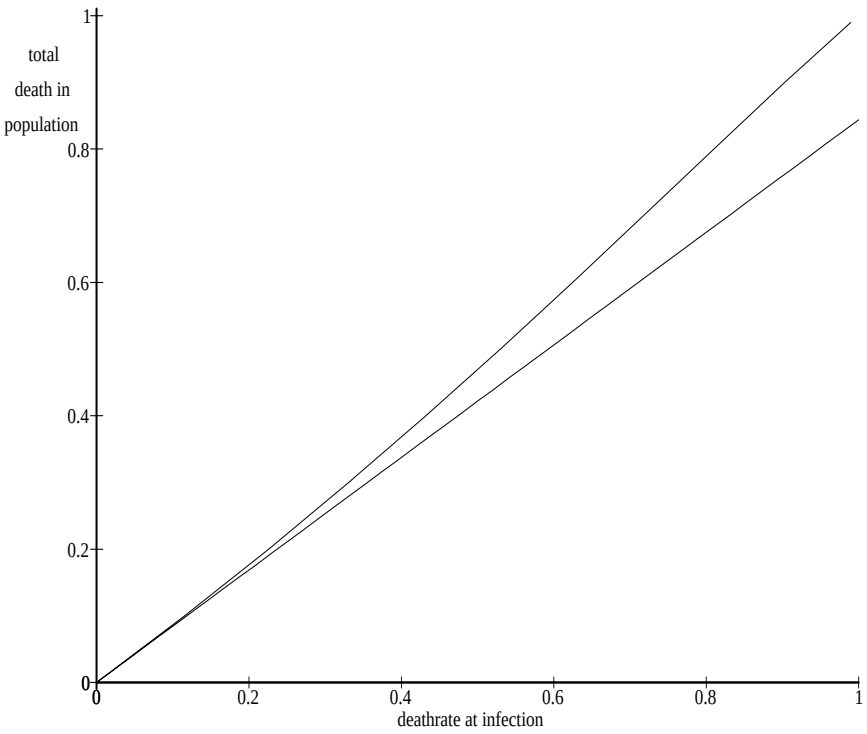

Figure 3. Total deaths in the population with different modelling assumptions while Ro=2.2.
The straight line takes only account of the direct effect, as it simply multiplies the final size for $f = 1$ by the probability $1 - f$ to die. The curved line gives the fraction of the population that dies from the disease, according to (2.10) and (2.11) and so takes account of both effects. We see that the indirect effect is quite important for low survival (i.e. when $1 - f$ is large)

6. TABLE

Values for f and R_0 in table 1-3 are calculated from x and y estimates. These estimates are taken from literature.

Location	x	y	f	R_0
a. Denmark [10]				
Koster	0.38	0.05	0.33	2.1
Varberg	.38			
Hesselø	.40	.01	.39	3.0
Anholt	.33	.03	.31	2.4
Måkläppen	.41	$<.03$	.4	>2.3
b. Kattegat and Waddensea area [17] *				
Netherlands	.44	.03	.42	2.5
Niedersachsen	.50	.03	.48	2.6
Schlesw.H	.39	.03	.37	2.3
Denmark	.49	.03	.47	2.6
c. Data from Dietz et al. and Grenfell et al. [6] [7]				
Kattegat/ Waddensea	.40	.03	.38	2.4
Kattegat/ Waddensea **	.40	.05	.37	2.1
East Anglia	.52	.05	.49	2.3
Irish sea	.60	.05	.58	2.5
Eastern Scotland	.95	.17	.94	2.1
Eastern Scotland **	.90	.16	.88	2.1

*) Data for x are from countings before and after the epidemic; y is the average from Denmark, table 1.
**) As the data are not always consistent for this area, two different estimates are considered.